

The intron sequences between exons 2 - 3 and exons 18 - 19 are missing (introns: small letters, exons: capital letters). Small letters in the first exon indicate nucleotides that have not been unambiguously determined.

Exon 1

```

1  CGGGTGAATC CCGGCGCCGC GCCCCGGACC CGCAGCTCCC TGCCTCCTC
51  CCTCCCAGCC GCTTTAACAC CCACACCCCA CAGTCTCTCC CACGsCCGCG
101 CCTTGGCGGC CCCACTGAAT CCCTACGCGG GGCCCAGCGG TACCGGGAGA
151 CCGGGCTAGC CTATGGGAGC GCCCAGATAA CGCGGGTTGG GGGCGCCCGC
201 GCCCCcATCC CCGCCAGCAAT GACTCGATCG CCGCCCCCTCA GAGAGCTGCC
251 CCCGAGTTAC ACACCCCCAG CTCGAACCGC AGCACCCAG gtgagtagag
301 ggggagctgg aagaaggaag agagcggagc caggtctgtc actcgggcct
351 ctgcaagggt tgtgatgtct tgaagtgccg agtgtcatta gatgtctgaa
401 ggcaagttag agccagcacc gcaagcaagt tgtgctgtgt tgtcgggtgtg
451 tctgtgccgg tgtctcctca tcgtctggcc agtgagaatg aatgtctgtg
501 ggttcacctc tgtgtccacc cgacgacagg tgtgtgtaca tatgtatcct
551 gctctcagaa aatgggccta tgccgccggg cgcggtgact cagcctgta
601 atcccaacac tgggaggtgt aggcaggcag attacctgag gtcaggagtt
651 cgagaccagc caggccaaca tggggaaact ctgtctctac taaaaataaa
701 aattagcagg gcgtggtggc gggcgctgt agtcccaact actcgggagg
751 ctgaggcagg agaattctct gaacctggga ggcggagggt gcagtcaagc
801 cgagatcaca ccaactgcact ccagccaggg caacagagcg agatgcgtct
851 caaaaaaaaa aaaaaaaaaa aaaaggagag aaaacaaaaa gaaaagaaag
901 gaaaataggc ctatgccttc ctcagggtgt tgcctgggat ggtgggtgtt
951 acatottcca agtctgggcc tgtgtctgtg ttggtgctcc ctgtoccaca
1001 tccagaaatc aagaagcgag ggctgggcag cagatataca gggtgagaag

```

Fig. 1

09807007-070901

WO 00/20037

PCT/SE99/01784

2/13

1051 ggaaggattt catgcattgt tacagtgatg cctggctgac ccttctcttt
EXON 2
1101 ccateccaga TCCTAGCTGG GAGCCTGAAG GCTCCACTCT GGCTTCGTGC
1151 TTACTTCCAG GGCCTGCTCT TCTCTCTGGG ATGCGGGATC CAGAGACATT
1201 GTGGCAAAGT GCTCTTCTG GGAAGTTGG CCTTTGGGGC CCTGGCATT
1251 GGTCTCCGA TGGCCATTAT TGAGACAAAC TTGGAACAGC TCTGGGTAGA
1301 AGTGGGAGGC CGGGTGAGCC AGGAGCTGCA TTACACCAAG GAGAAGCTGG
1351 GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGAC CGCACGCCAG
1401 GAGGGAGAGA ACATCCTCAC ACCCGAAGCA CTTGGCCTCC ACCTCCAGGC
1451 AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAG.....
1501g
1551 tgagtctggc tgagcccctg agcagctggg ggcgaggcgt gctgtggggg
1601 ttctggagtg ggaatcccct tcttctgctg atctctctatg cccctggcta
EXON 4
1651 ttgcagTCCT GGGATTGAA CAAAATCTGC TACAAGTCAG GAGTTCCCCCT
1701 TATTGAAAT GGAATGATTG AGCGGgtaag tgcctgaga gggagtagag
1751 gcagaacttt ttctgtagcg tgggaggact cagagaccga gcaagcccca
1801 cagcctgcaa tctgccccct taaaactaag gagggggatt gcagagggca
1851 tcctacaaag gttgtggggc aggactgacg tggcccgggg tatccctggc
EXON 5
1901 agATGATTGA GAAGCTGTTT CCGTGCGTGA TCCTCACCCC CCTCGACTGC
1951 TTCTGGGAGG GAGCCAACT CCAAGGGGGC TCCGCCTACC TGCCgtgagt
2001 gccactcctg gggccctgct tcctctcccg ctggggactc tcccagcaga
2051 aaggaggggt ctggggaatg aggatgatca aaaccttacc aaggctcctaa
2101 ttacctccca ggccaggaac agagagcatg ggcttcccca aggctctctc
2151 cacatcctcc ttctctttcc ctctcaagga aggaagacct gacttattta
2201 cacaaaacta aacacaaaga tctgtaagat ctgagcaaag gagaaaaaga
2251 tccccacaaa gaggctttgc tgggggaaat tacctaggtg tttgctaagc
2301 cattgcccag gccagaaaga aaacctgcta caggcatgtg cctgetgggt
2351 gtatattaga accaagcaca cagcttggtg aggaactcag tggggccttt

Fig. 1 (cont.)

T06020" 20040860

WO 00/20037

PCT/SE99/01784

3/13

2401 ctggggccctt tctatgtatt aggtaaccct gccctgatat t⁻cgctctcagc
 2451 cccttggtact cttctacagc tcaactgtagc accctgggtgg gcccattgcag
 2501 cctggcagtt ctgagaagct gaggcttgca caccctccat atggaaggac
 2551 aaatcggcag ataagaggag ggtggggtac agcatggcgc ccagcagca
 2601 gtttggagcc tgggttttcg tccctgacct tcaccaacta taggcttttc
 2651 cctcagCGGC CGCCCGGATA TCCAGTGGAC CAACCTGGAT CCAGAGCAGC
 2701 TGCTGGAGGA GCTGGGTCCC TTTGCCTCCC TTGAGGGCTT CCGGGAGCTG
 2751 CTAGACAAGG CACAGGTGGG CCAGGCCTAC GTGGGGCGGC CCTGTCTGCA
 2801 CCCTGATGAC CTCCACTGCC CACCTAGTGC CCCCACCAT CACAGCAGGC
 2851 AGgtgggttc caaccaggtc tgccagggaa aggctgtttt ccttcccttt
 2901 cccttctca tactcctgtg ttctggggga gctgactgct ctgtgccctg
 2951 accccccaact tcctggccat tattaccctg ctcccacagt gccaggcccc
 3001 caatgttcca ttcccattca gttatcctac ggagccctca agtgggtatat
 3051 atgaatccct ttttcctttt ctaagcctag ataaggctgg acttcttttt
 3101 tttttttttt ttgagtctca ctctgtcacc caggctggag tgcagtagtt
 3151 cgatcttggc tcaactgcaac ctcggtcaa gcaattctcc tgccttagcc
 3201 tcctgagtag ctgggattac aggtgccac caccatgcc ggctaatttt
 3251 tattagcctc ccaaagtgt gggattacag gcgtgagcca ctgcgcctgg
 3301 ccaaggctgg actttttatc aaaatagact aatacagga aactaagaac
 3351 acagcaggta agcatgaata tcatacctgg tttcccaggt ttctttgtgg
 3401 ccctgcaaat gtggtacttt tttcagaatc cgccagttac accagctcct
 3451 ccagaagcc tacttccagg cctctgcttc cccttggggc ttctgtctg
 3501 cgggatacta gctgttcaact cctgcagagc agtcaagagg ctccagaatag
 3551 ttacctacac tccagcccta ctgagcttca tggcagcgtg gttcctggag
 3601 gtggaagccc agggacactc agttatccac ggccagggcc ttgagcatta
 3651 acccctcctg ttccccctca GGGCTCCCAA TGTGGCTCAC GAGCTGAGTG
 3701 GGGGCTGCCA TGGCTTCTCC CACAAATTCA TGCACTGGCA GGAGGAATTG

Fig. 1 (cont.)

09807007.070901

WO 00/20037

PCT/SE99/01784

4/13

3751 CTGCTGGGAG GCATGGCCAG AGACCCCCAA GGAGAGCTGC TGAG⁻Gtaggg
 3801 tctcctctgg gagttggtga ggggactctg ttcattgagaa cccatactgt
 3851 aatgccagge agctctggca aaaggccctt cacatccctc accaggtgtt
 3901 tggggccagct ctgacccttg gttctccac acccccacca gGGCAGAGGC
 3951 CCTGCAGAGC ACCTTCTTGC TGATGAGTCC CCGCCAGCTG TACGAGCATT
 4001 TCCGGGGTGA CTATCAGACA CATGACATTG GCTGGAGTGA GGAGCAGGCC
 4051 AGCACAGTGC TACAAGCCTG GCAGCGGCGC TTTGTGCAGg tgggtatgga
 4101 caaggacaag gggggtgccc tgaggccatt cctcctcct gccccctcct
 4151 atccaccctg tttctccagc TGGCCCAGGA GGCCCTGCCT GAGAACGCTT
 4201 CCCAGCAGAT CCATGCCTTC TCCTCCACCA CCCTGGATGA CATCCTGCAT
 4251 GCGTTCTCTG AAGTCAGTGC TGCCCGTGTG GTGGGAGGCT ATCTGCTCAT
 4301 Ggtgggtcctt gcacctggca cettgcccc accccacctc caaccagtgc
 4351 ccacctggg agccccctgag actgcccctt cccccacag CTGGCCTATG
 4401 CCTGTGTGAC CATGCTGCGG TGGGACTGCG CCCAGTCCCA GGGTTCCGTG
 4451 GGCCCTGCCG GGGTACTGCT GGTGGCCCTG GCGGTGGCCT CAGGCCTTGG
 4501 GCTCTGTGCC CTGCTCGGCA TCACCTTCAA TGCTGCCACT ACCCAGgtac
 4551 gccaggactg cagggcagac tcagtgccag tcaccaggct tcacgggtcc
 4601 tcagctgccc gctcctctgc cctccagGT GCTGCCCTTC TTGGCTCTGG
 4651 GAATCGGCGT GGATGACGTA TTCCTGCTGG CGCATGCCTT CACAGAGGCT
 4701 CTGCCTGGCA CCCCTCTCCA Ggtggggcct tgtccccag ggctcatctg
 4751 aggcagctca gcttactggt taagagcctc ttggttcaag tgacccttgg
 4801 gctgctaatag aacctcgggt cctctgtcc ccatctgtaa acaggggaaa
 4851 taatagtgt gtgtcctaag ggttattgtt tggatcagtg aggtaactca
 4901 agttgaatgc ttagaacagc ccatcatag tacatggtac ccaataaatg
 4951 ctageccactg tgttatgact gccccacctc tgcaccccaa gttcctgagc
 5001 ctcccccttca ctccactttg acacggcccc tcccttgtga cctgagggca
 5051 ggtccccact ctgtcctggc agGAGCGCAT GGGCGAGTGT CTGCAGCGCA

Fig. 1 (cont.)

09807007.070901

5/13

5101 CGGGCACCAG TGTCGTACTC ACATCCATCA ACAACATGGC CGCCTTCCTC
 5151 ATGGCTGCCC TCGTTCCCAT CCCTGCGCTG CGAGCCTTCT CCCTACAGGC
 5201 GGCCATAGTG GTTGGCTGCA CCTTTGTAGC CGTGATGCTT GTCTTCCCAG
 5251 CCATCCTCAG CCTGGACCTA CGGCGGCGCC ACTGCCAGCG CCTTGATGTG
 5301 CTCTGCTGCT TCTCCAGgta ctgcggtgogc cccagccct tctctccgtg
 5351 acccacgcca gcctgtcccc tcaccagcat ttcaaggcac agacctgtca
 5401 tccactctct acctcttcca gTCCCTGCTC TGCTCAGGTG ATTCAGATCC
 EXON 13
 5451 TGCCCCAGGA GCTGGGGGAC GGGACAGTAC CAGTGGGCAT TGCCCCACCTC
 5501 ACTGCCACAG TTCAAGCCTT TACCCACTGT GAAGCCAGCA GCCAGCATGT
 5551 GGTCAACATC CTGCCTCCCC AAGCCCACCT GGTGCCCCCA CCTTCTGACC
 5601 CACTGGGCTC TGAGCTCTTC AGCCCTGGAG GGTCCACACG GGACCTTCTA
 5651 GGCCAGGAGG AGGAGACAAG GCAGAAGGCA GCCTGCAAGT CCCTGCCCTG
 5701 TGCCCGCTGG AATCTTGCCC ATTTGCGCCG CTATCAGTTT GCCCCGTTGC
 5751 TGCTCCAGTC ACATGCTAAG gtaagactgg gcagagcagg gcagagactt
 5801 agcatctctg ggcccagaag ggcagagagg gcttagtcca ctgcctgagg
 5851 ggctgggggc agccctgggg tctccagctt agttgctaca tcccgcagGC
 EXON 14
 5901 CATCGTGCTG GTGCTCTTTG GTGCTCTTCT GGGCCTGAGC CTCTACGGAG
 5951 CCACCTTGGT GCAAGACGGC CTGGCCCTGA CGGATGTGGT GCCTCGGGGC
 6001 ACCAAGGAGC ATGCCTTCCT GAGCGCCCAG CTCAGGTACT TCTCCCTGTA
 6051 CGAGGTGGCC CTGGTGACCC AGGGTGGCTT TGA CTACGCC CACTCCCAAC
 6101 GCGCCCTCTT TGATCTGCAC CAGCGCTTCA GTTCCCTCAA GGCGGTGCTG
 6151 CCCCCACCGG CCACCCAGGC ACCCCGCACC TGGCTGCACT ATTACCGCAA
 6201 CTGGCTACAG Ggtgagaggg gaggagacgg gcagggaggg gtgctgcagg
 6251 gagaaacgcc ctggggccac cagctaataa aaccctatcc tgggtctcccc
 EXON 15
 6301 cagGAATCCA GGCTGCCTTT GACCAGGACT GGGCTTCTGG GCGCATCACC
 6351 CGCCACTCGA CCGCAATGGC TCTGAGGATG GGGCCCTGGC CTACAAGCTG
 6401 CTCATCCAGA CTGGAGACGC CCAGGAGCTT CTGGATTTCa GCCAGgttgg

Fig. 1 (cont.)

09807007-070901

6/13

6451 gagagggctg gaggggtcca ctagtacagg ggctgcaggc ctcctgggccc
 6501 caggccttca gccctctctg cctctgcagC TGACCACAAG GAAGCTGGTG
 6551 GACAGAGAGG GACTGATTCC ACCCGAGCTC TTCTACATGG GGCTGACCGT
 6601 GTGGGTGAGC AGTGACCCCC TGGGTCTGGC AGCCTCACAG GCCAACTTCT
 6651 ACCCCCCACC TCCTGAATGG CTGCACGACA AATACGACAC CACGGGGGAG
 6701 AACTTTTCGCA gtgagtcttg gggggagctc ggcaagagcc tcagcctcgc
 6751 ccacacaagc cctgagcctg aggccctgcc cactctgccc cgtgctcacc
 6801 gccctgtccc tctccctctt ctcccttccc ctccctccca cagTCCCGCC
 6851 AGCTCAGCCC TTGGAGTTTG CCCAGTTCCC TTTCCTGCTG CGTGGCCTCC
 6901 AGAAGACTGC AGACTTTGTG GAGGCCATCG AGGGGGCCCG GGCAGCATGC
 6951 GCAGAGGCCG GCCAGGCTGG GGTGCACGCC TACCCAGCG GCTCCCCCTT
 7001 CCTCTTCTGG GAACAGTATC TGGGCCTGCG GCGCTGCTTC CTGCTGGCCG
 7051 TCTGCATCCT GCTGGTGTGC ACTTTCCTCG TCTGTGCTCT GCTGCTCCTC
 7101 AACCCTTGGA CGGCTGGCCT CATAgtagt gcttgcagga gtggggacag
 7151 agacacccca cccttccctg cccagcctgt catccctcct gccaggagcc
 7201 ctctgtgagc cctgtctccc tcagGTGCTG GTCCTGGCGA TGATGACAGT
 7251 GGAACCTCTT GGTATCATGG GTTTCCTGGG CATCAAGCTG AGTGCCATCC
 7301 CCGTGGTGAT CTTGTGGCC TCTGTAGGCA TTGGCGTTGA GTTCACAGTC
 7351 CACGTGGCTC TGGGCTTCCT GACCACCCAG GGCAGCCGGA ACCTGCGGGC
 7401 CGCCCATGCC CTTGAGCACA CATTGCCCC CGTGACCGAT GGGGCCATCT
 7451 CCACATTGCT GGGTCTGCTC ATGCTTGCTG GTTCCCACTT TGAATTTCATT
 7501 GTAAG.....
 7551 gtagggaggg ctcggggcag ggaggcaggg ctcaggacag
 7601 gcctgggctg actcccccca caccctaccc ctagGTACTT CTTTGCGGCG
 7651 CTGACAGTGC TCACGCTCCT GGGCCTCCTC CATGGACTCG TGCTGCTGCC
 7701 TGTGCTGCTG TCCATCCTGG GCCCGCCGCC AGAGgtgacc acaccctcgg
 7751 caccatccct ctactcccag cccaaggagc ggggtaggga gaggcaaggg

Fig. 1 (cont.)

T05020 20020360

WO 00/20037

PCT/SE99/01784

7/13

7801 aagggacaga gccctgtggc ccacagacag gtacctcccc aacaggtgcc
 7851 accagctgaa ggtggcagcc tcctcctttc ccagacacc atgttcctgc
 7901 ccctcagccc tcctggcttc ttcattgggac ccaccttaga cttttaggat
 7951 ccagaacaag gtgcagggtt tgccccaggc ctcaacatcc tgtgcctgc
 8001 cagctctcat atcctgctgg agaccaacaa gggccccagc ttcccaacag
 8051 tcatggtaat cccagcgag atgctaaagg ggacgggagc cccagggggc
 8101 cgtgggctta ctggggctgg tgtctcccca cagGTGATAC AGATGTACAA
 8151 GGAAAGCCCA GAGATCCTGA GTCCACCAGC TCCACAGGGA GCGGGGCTTA
 8201 Ggtggggggc atcctcctcc ctgccccaga gctttgccag agtgactacc
 8251 tccatgaccg tggccatcca cccaccccc ctgctggtg cctacatcca
 8301 tccagccct gatgagcccc cttggctccc tgcctgact agctctggca
 8351 acctcagttc caggggacca ggtccagcca ctgggtgaaa gagcagctga
 8401 agcacagaga ccatgtgtgg ggcgtgtggg gtcactggga agcactgggt
 8451 ctgggtgttag acgcaggatg gaccctgga gggctctgct gctgctgcat
 8501 cccctctccc gaccagctg tcatgggcct cctgatatc catacagaac
 8551 agccaccgat ttgcacatcc aggcctgtgt gagcctgtat ctgtgtcact
 8601 tgagagtga agetggcact tggggctgca gtgcagccct gtcccccttc
 8651 ccaccccaca cactgcctg cccagctgac caagcctgag ggaacctcca
 8701 gcacccttcc gtctgggtgac tcctgggcag gctctccata tccctgccc
 8751 cctcctacca catccattat ttatatgaaa atgtctattt ttgtagtata
 8801 catacatgtt agctatgatg aaagttttat tttttaaaga atgaaatata
 8851 ttctatgtga agctatgatg aaagttttat tttttaaaga atgaaatata
 8901 ttctatgtga actaatctcg aaagttttat tttttaaaga atgaaatata
 8951 ttctatgtgt gcaagtgaac attagcttca gttgcttttt tttggacaga
 9001 gtggggagtt tgcaagtga cattaactat tggaaggagc ttctctgggtg
 9051 ccaggacctg aggtattagc ttctctagtt ctgggtggaa aagacccag
 9101 attctggatt tttgtcatat acttggtaac atcatctgga ttaagtgcct

Fig. 1 (cont.)

09807007-0009901

8/13

9151 actatacaaa acgataacaa attttgttgg tgtgaaatcc tactgggttc
 9201 aatctggaga ccgagagcag aaaaaaaga accccactgt gtggctttca
 9251 gagccaccat attccagcct gccgtctct ccagactcac ctccacctac
 9301 ctgcttcacc cgcacgggaa acggcaaggc agaggggcaa agccatgcag
 9351 caggtggaag gcgaggtgga ggcagatcag gaaagcagcc agttgaagca
 9401 gagagaggtc aacaggggtct ggggagcttc tcaggaggtt tgtggacca
 9451 gggaaaggag ccaggttcca gagcaacctc caaggcaaag gcctctgtaa
 9501 gttggttgtc ctgacagccg agaggtgtct ttggccagtc agccagtga
 9551 tcagttgcgg gaactgctca gaaactgagg tgctagcagt tagtgaggac
 9601 acagcgtaag ttgtttgttc tgtgaaagtt gaacagctcc actaagcaga
 9651 ggccttgaag agtggccaca gccctggaat agagcacaga gcctcaccta
 9701 gaggcgtggg gaggtttgca actgcccctt cccagccata gcttaggacc
 9751 catagtctag ttcacataga ccctgggctc caaccacca ctcaccagga
 9801 atgatccac cccaggaaca atgcgttctc acatcccacc ccacctggac
 9851 aaaggccagg aatcatgtt ctgacaaaaa gatacaacaa caaaaacaac
 9901 aacaacaaaa aacgcctatt gcaattgaat ccacgctaaa atgcctaaaa
 9951 agctcaagag aagcgggtag ttggcagaga acctagagta ggggggtgcaa
 10001 ccagcaggcc caagggaggg aggctgcatt tgggtccagc agtgtttggg
 10051 tcaccaagaa gggccttcta ggtggagcag agagagctca ccaggccaga
 10101 atagtcaaaa gggggtcagc cctcagtgc acttaccagc ggagtaacc
 10151 tgggcaagtt agccagcctc actaagcctc cccatcttca tctttccagG
 XON 22
 10201 CCCGAGGAGA TC**TAG**CCTCT GCCTCCCACC CCAGCACCCC CTCATCAGAC
 10251 ACAAGGAGCG CCACTGTCTG GACAGGCTGA ATTGGTCTTC GGGTCCCTAA
 10301 TTTCTCATAC GCCATTCCCT CTGCCTAGAA CACTTTCTCA CCTCCCCTTG
 10351 ATGTGACCCC ATATCACCCCT TCGAGGTGAA TTGGATCGGA TGCCATCTCC
 10401 TCCAGGAGGG GTGGGGTCGT GCCTCCTGTG AGGTCCCAGT GCCCCTGAGT
 10451 GTCTGTGCCC GTCTGTTTCC CCGTCCCTCT CTCTAAGCCC GGAGGCTTAC

Fig. 1 (cont.)

09807007.070901

WO 00/20037

PCT/SE99/01784

9/13

10501 TCGGGGTAAG GACGGCGGGA CAGGACCTTA ACCGCTGGGA CGAACACCAG
10551 CTCCGCAAAG GACTCCGCAC CCGGCGCCGC CCACGGGGTG CGGGTCCCAG
10601 GAGGACCAGC AGAGAGGAGC ATAGGAGAGC AAAGGAGATC AGTGACCCAT
10651 GGCTTCCCCG GTGGCGCGGA ACAGCCCGGA GCCGCCTGTG ATTTGCATAC
10701 CCATGGTGCA CCACGAAAAG ATACCCTCAA GATGCTTGCA CTCCCTCTGT
10751 GCGCGCATTT CTGCACTGTT TTAGAGCATG ATGCCTCTTA CACGCATCTG
10801 TGTGCATAAA CTACATATAG GGAGTGCGTA CCACGCAGGC ATCCAACAAC
10851 CATAAGTGTG TTAAGTGTTA GTTCTCCCTG CGAGGTTCGA AGCGGAAGTC
10901 ACGAATATAC TCGGGTTTCT CTTCAAAGCG CATAAATCTT TCGCCTTTTA
10951 CTAAAGATTT CCGTGGAGAG AAAGTTGTGA GTTTTTATTTC AATTTTTTGA
11001 GGCCTCTTAT TTCCTGAGGC TACATTTTAA AGTATTAAAA GTTAGGCAAC
11051 TACAAAAAAA AAAAAAAA

Fig. 1 (cont.)

09807007 20020860

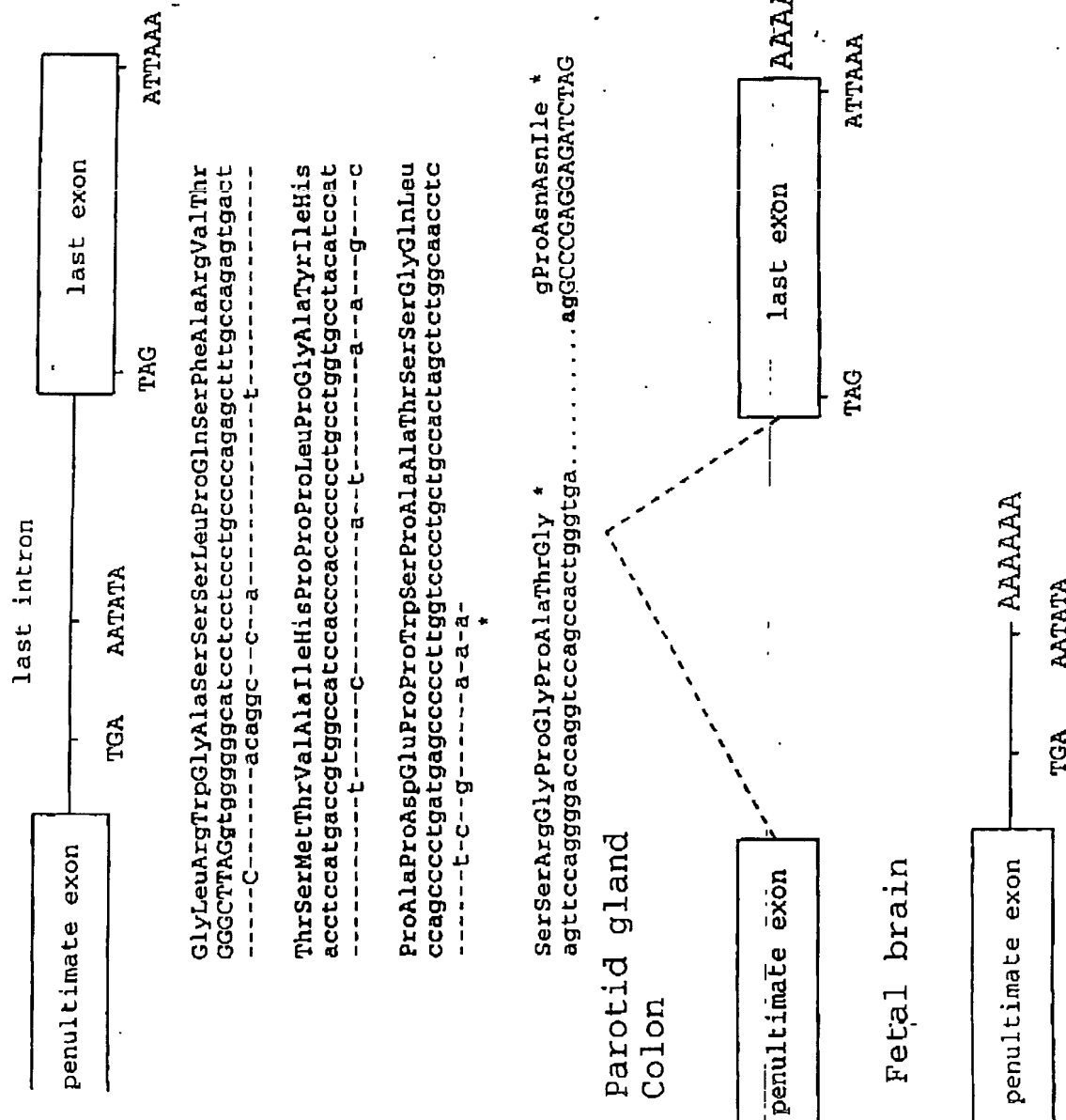
10/13

1MTRSPPLRELE..... 11
 1 MASAGNAAEPQDRGGGSGCIGAPGRPAGGGRRRTGGLRRAAPDRDYL 50
 12 ..PSYTPPARTAAPQI...LAGSLKAPLWLRAYFQGLLFSLGCGIQRHCG 56
 51 HRPSYCDAA.FALEQISKGKATGRKAPLWLRKFQRLLEFKLGCYIQKNCG 99
 57 KVLFLGLLAFGALALGLRMAIETNLEQLWVEVGSRVSQELHYTKKLG 106
 100 KFLVVGLLIFGAFVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGE 149
 107 EAAVTSQMLIQATARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDL 156
 150 EAMFNPQLMIQTTPKEEGANVLTTEALLQHLDSALQASRVHVVMYNRQWKL 199
 157 NKICYKSGVPLIENGMIERMIEKLPFCVILTPLDCFWEAKLOGGSAYLP 206
 200 EHLCKYSGELITETGYMDQIIEYLYPCLIIITPLDCFWEAKLOGSTAYLL 249
 207 GRPDIQWTNLDPEQLLEELGPFA.SLEGFRELLDKAQVGQAYVGRPCLHP 255
 250 GKPLLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGYMDRPCINP 299
 256 DDLHCPPSAENHHSRQAPNVAHELSSGCHGFSHKFMHWQEELLLGGMARD 305
 300 ADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKN 349
 306 PQGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAW 355
 350 STGKLVSAAHALQTMFQLMTPKQMYEHFKGYEYVSHINWNEDKAAAILEAW 399
 356 QRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVGGYLLM 405
 400 QRTYVEVVHQSVAQNSTQKVLSTTTTLDDILKSPSDSVIKVASGYLLM 449
 406 LAYACVTMLRWDCAQSGSVGLAGVLLVALAVASGLGLCALLGITFNAAT 455
 450 LAYACLTMLRWDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAAT 499
 456 TQVLPFLALGIGVDDVFLLAHAFTEALPG..TPLQERMGECLQRTGTSVV 503
 500 TQVLPFLALGVGVDDVFLLAHAFSETGQNKRIPFEDRTGECLKRTGASVA 549
 504 LTSINNMAAFLMAALVPIPALRAFSLOAAIVVGCTFVAVMLVFPAILSLD 553
 550 LTSISNVTAFMAALIPIPALRAFSLOAAVVVFNFAMVLLIFPAILSMD 599
 554 LRRRHCQRLDVLCCFSSPCSAQVIQILPOELGDGT.....VPVG 592
 600 LYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDHNTYSPPPYSSHS 649
 593 IAH.....LTATVQAFTHCEASSQHVVITLPPQAH.....VPPPSDPLGS 633
 650 FAHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVITVQDTLSC 699

Fig. 2A

T06020" 20020360

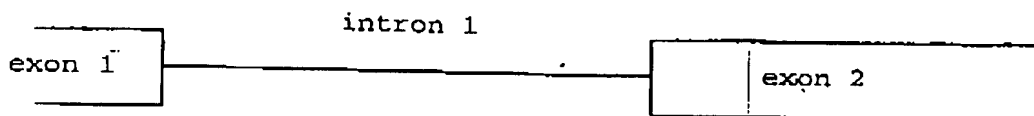
Fig. 2B Genomic



12/13

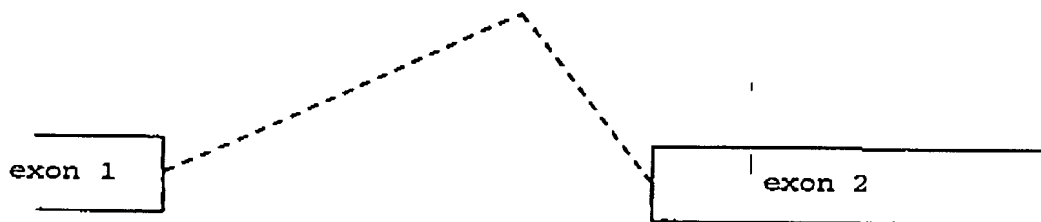
Fig. 2C

G



Pro Gln Ile Leu Gln Gly
 CCC CAG gt.....gt.....ag ATC CTA.....Cag GGC
 ← 67 bp → ← 755 bp → 51 bp →

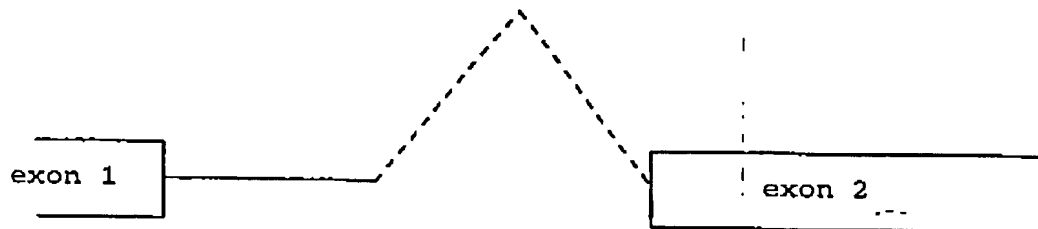
C



A



B



09807007 20040860

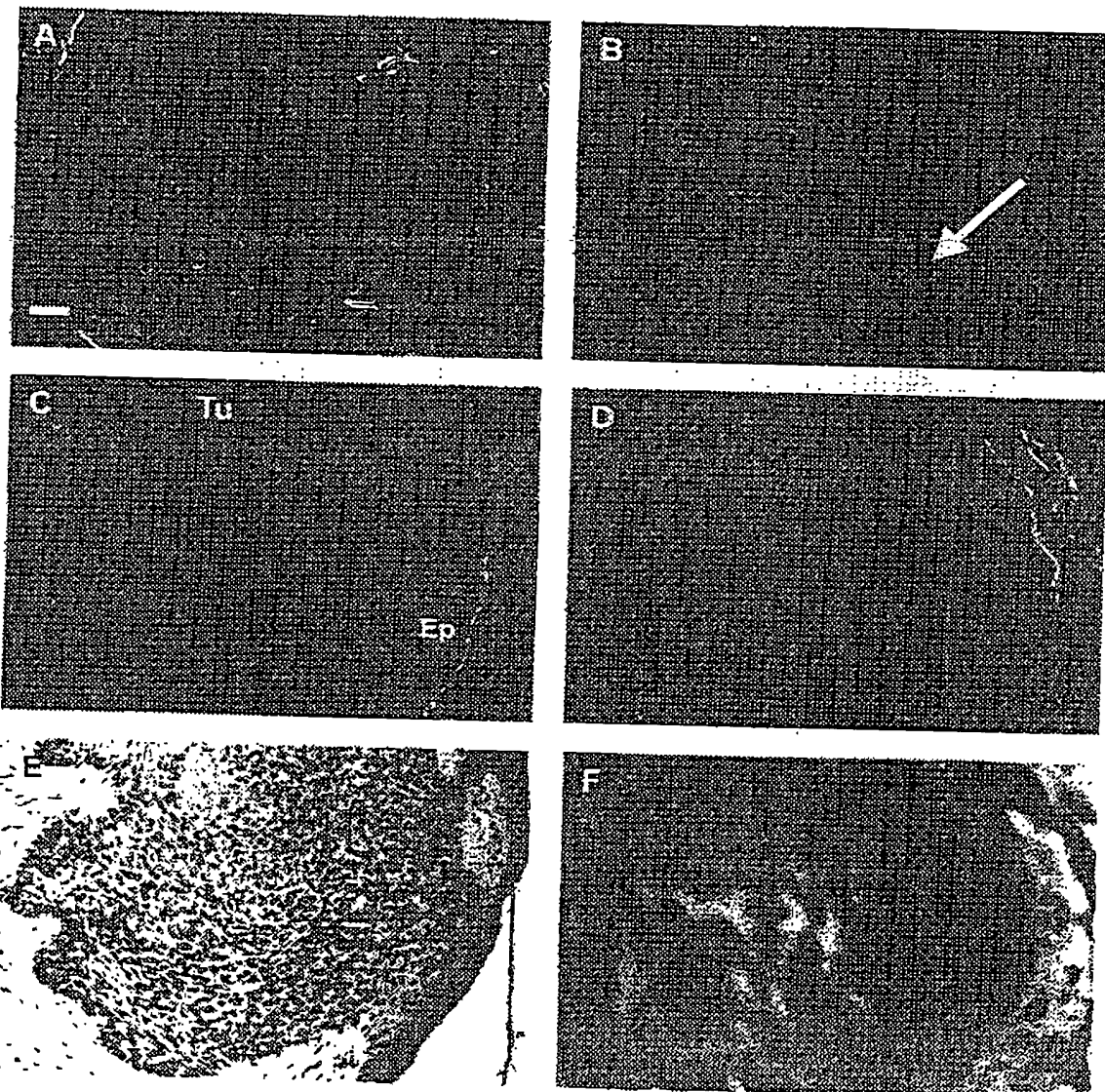


Fig. 3